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A new species of *Plagiopholis* Boulenger, 1893 (Serpentes, Pseudoxenodontidae) from Guangdong, China

Shuo Qi[1], Han-Ming Song[1], Hao-Cong Yang[1], Yu-Hao Xu[2], Rui-Jian Fang[3], Jun-Rong Su[4], Zhi-Fa Liu[5], Yue-Ning Gong[5], Fang-Hua Li[6], Chun-He Lyu[7], Bing-Yang Wang[8], Ying-Yong Wang[1]

1 *School of Ecology / School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, Guangdong, China*
2 *State Key Laboratory of Plateau Ecology and Agriculture, Qinghai University, Xining, 810016, Qinghai, China*
3 *No. 42, Qiaole Road, Xiqiao Town, Nanhai District, Foshan 528211, Guangdong, China*
4 *Foshan Nature Fenxiangshe Nature Science Popularization Co., Foshan 528500, Guangdong, China*
5 *Administration of Guangdong Nanling National Nature Reserve, Shaoguan 512000, Guangdong, China*
6 *Administration of Guangdong Tianjingshan National Nature Park, Shaoguan 512726, Guangdong, China*
7 *Forest Resources Conservation Center of Guangdong Province, Guangzhou 510173, Guangdong, China*
8 *Guangdong Wildlife Rescue and Monitoring Center, Guangzhou 510520, Guangdong, China*

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Corresponding authors: Shuo Qi (qishuo1992@outlook.com); Ying-Yong Wang (wangyy@mail.sysu.edu.cn)

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Abstract

The genus *Plagiopholis* Boulenger, 1893 is a poorly studied genus from the Oriental realm, currently comprising six recognized species. We herein describe a new species of the genus, *Plagiopholis maculosa* **sp. nov.** from Guangdong Province, China. A morphological examination combined with two mitochondrial gene fragments (CO1 and cyt *b*), was used to test its distinctiveness within *Plagiopholis*. Morphologically, the new species differs from other congeners by the following diagnostic characteristics: no loreal; temporals 2+2; maxillary teeth 17; 104 ventrals, excluding two preventrals; 24 pairs of subcaudals, excluding the tail tip; presence of a large inverted "V"-shaped nuchal blotch; and a series of distinctive irregular blotches on the dorsum. The phylogenetic analyses shows that the new species exhibits pronounced genetic divergence from all recognized congeners (12.73%–15.88% in CO1, 16.17%–17.54% in cyt *b*). This discovery increases the number of valid species in the genus *Plagiopholis* to seven. Moreover, the extensive sampling gaps across its distribution suggest that additional cryptic species may remain to be discovered.

Key Words

Mountain Snakes, morphology, Nanling Mountains, *Plagiopholis maculosa* sp. nov., taxonomy

Introduction

Plagiopholis Boulenger, 1893, commonly known as the mountain snakes, is a poorly studied genus of small, semi-fossorial, non-venomous snakes, distributed in southern China, Myanmar, Laos, Vietnam and the central and northern parts of Thailand (Zhao 2006; Cai et al. 2025; Uetz et al. 2025). Although species of the genus *Plagiopholis* have a relatively wide distribution, specimens are rarely collected due to their cryptic habits. Consequently, for a long time, research on *Plagiopholis* relied exclusively on morphological data, until Zhong et al. (2015) provided molecular sequences for the genus by placing *P. unipostocularis* Zhao & Huang, 1979 in synonymy with *P. blakewayi* Boulenger, 1893. Nevertheless, comprehensive phylogenetic and biogeographic assessments of the genus remain hindered by substantial sampling gaps. Recently, two taxonomic studies provided molecular sequences of the topotypic material of *P. styani* (Boulenger, 1899), which enabled the recognition of additional cryptic lin-

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eages within *Plagiopholis*. In the same context, two new species from China were described and the distribution range of *P. styani* was revised (Cai et al. 2025; Liu et al. 2025). This brings the total number of valid species in the genus to six: *P. acuta* Xu, Ma & Cai, 2025, *P. blakewayi*, *P. delacouri* Angel, 1929, *P. nuchalis* (Boulenger, 1893), *P. pluvialis* Cai, Xu & Ma, 2025, and *P. styani*. Among these, all species except *P. delacouri* occur in China.

Historically, records of *Plagiopholis* from Guangdong Province, China have been sparse. Mell (1929) hypothesized that *Trirhinopholis styani* might occur in northern Guangdong near the border with Jiangxi. The first formal record was reported by Liang (2003), who identified a specimen from the Nanling National Nature Reserve as *Plagiopholis styani*. In the more than two decades since, only a few sighting records have been documented, but no additional specimens have been obtained.

During recent herpetological surveys in Tianjingshan National Forest Park, Nanling National Nature Reserve, one snake specimen was collected. Detailed morphological examinations and further molecular analyses revealed that this specimen represented a separately evolving lineage within the genus *Plagiopholis* which can be distinguished from all recognized congeners. In light of these findings, we provide a detailed description of the new species herein.

Materials and methods

Morphometrics

Morphological examinations were performed on a single specimen collected from Tianjingshan National Forest Park, Ruyuan County, Shaoguan City, Guangdong Province, China (Fig. 1). The specimen was fixed in 10% buffered formalin after taking the tissue samples (liver and muscle), and then transferred to 70% ethanol for permanent preservation. The specimens are deposited in the Museum of Biology, Sun Yat-sen University (SYS r002979).

Morphological descriptions follow Dowling (1951) and Zhao (2006). The following measurements were taken with digital calipers (Neiko 01407A Stainless Steel 6-Inch Digital Caliper, USA) to the nearest 0.1 mm: **TL** total length (from tip of snout to tip of tail); **SVL** snout-vent length (from tip of snout to posterior margin of cloacal plate); **TaL** tail length (from posterior margin of cloacal plate to tip of tail); **HL** head length (from tip of snout to posterior margin of the mandible); **HW** maximum head width; **ED** eye horizontal diameter.

Scalation features and their abbreviations are as follows: **DSR** dorsal scale rows, counted at one head length behind head, at midbody, and at one head length before

Figure 1. The type locality of *Plagiopholis maculosa* sp. nov. and previously recorded locality of *Plagiopholis* cf. *styani* in Guangdong Province, China.

vent; **SPL** supralabials; **IFL** infralabials; **CS** chin shields; **PrO** preoculars; **PtO** postoculars; **LoR** loreal; **TMP** temporals; **V** ventral scales; **PrC** precloacal plate; **SC** subcaudals. Gender was determined by dissection or by the presence/absence of everted hemipenes. The numbers of maxillary teeth (**MT**) were counted by carefully dissecting the gums of the right maxilla under the stereo microscope.

Laboratory methods

Total genomic DNA was extracted from the liver tissue sample using the TIANamp Genomic DNA Kit (Tiangen Biotech Co., Ltd, Beijing). Two mitochondrial gene fragments, the partial cytochrome c oxidase subunit 1 gene (CO1) and the partial cytochrome b gene (cyt *b*), were amplified using the polymerase chain reaction (PCR). For PCR experiments, the primers and conditions followed Cai et al. (2025). After spin column purification, PCR products were sequenced by Tianyi Huiyuan Biotech Co., Ltd, Wuhan using forward primers on an ABI 3730 automated genetic analyzer.

Molecular phylogenetic analysis

A total of 26 samples, comprising six *Plagiopholis* species and an outgroup *Pseudoxenodon bambusicola* Vogt, 1922, were included in the phylogenetic analyses (Table 1). Among them, newly sequenced data have been deposited in GenBase (https://ngdc.cncb.ac.cn/genbase), and all other sequences were downloaded from GenBank (https://www.ncbi.nlm.nih.gov/genbank). All sequences were aligned using the MAFFT (Multiple Alignment using Fast Fourier Transform) algorithm with default parameters in MAFFT v7.037b (Katoh and Standley 2013), edited in order and concatenated seriatim as a final dataset of 1632 bp (605 bp for CO1 and 1027 bp for cyt *b*) in MEGA 11 (Tamura et al. 2021). Then the dataset was analyzed using the methods of Bayesian Inference (BI) and Maximum Likelihood (ML) in MrBayes 3.2.4 (Ronquist et al. 2012) and IQ-TREE 2.2.2.6 (Minh et al. 2020), respectively. For the BI analysis, two independent runs of 200,000,000 generations of Markov chain Monte Carlo each were performed with default parameters using the following settings: sampling every 1000 generations with the final 25% samples from the beginning discarded as burn-in, resulting in a potential scale reduction factor less than 0.005. For the ML analysis, the best substitution model for the whole dataset was chosen using ModelFinder based on Bayesian information criteria (Kalyaanamoorthy et al. 2017), and a consensus tree was inferred from 1000 replicates each of the ultrafast bootstrap and SH-aLRT (approximate likelihood ratio test) (Anisimova et al. 2011; Minh et al. 2013). Node support was evaluated using Bayesian posterior probabilities (BPP), ultrafast bootstrap (UFB) values, and SH-aLRT values. Nodes with BPP $\geq$ 0.95, UFB $\geq$ 95, and SH-aLRT $\geq$ 80 were considered strongly supported. Pairwise genetic distances were calculated in MEGA 11 (Tamura et al. 2021) for CO1 and cyt *b* respectively using the Kimura 2-parameter model with default options. The final alignment matrix consisted of 605 bp from 22 sequences for CO1 and 1027 bp from 24 sequences for cyt *b*.

Table 1. Sample list of the genus *Plagiopholis* and outgroup for phylogenetic analysis in this study.

	Species	Voucher	Locality	CO1	Cyt b	Reference
1	*Plagiopholis maculosa* sp. nov.	SYS r002979	China: Guangdong: Ruyuan: Mt. Tianjing	C_AA125965	C_AA126388	This study
2	*Plagiopholis acuta*	QHU 2024009	China: Hunan: Xinshao	PV335150	PV340623	Cai et al. 2025
3	*Plagiopholis acuta*	QHU 2024011	China: Hunan: Xinshao	PV335152	PV340625	Cai et al. 2025
4	*Plagiopholis acuta*	QHU 2024012	China: Hunan: Xinshao	PV335153	PV340626	Cai et al. 2025
5	*Plagiopholis acuta*	QHU 2024044	China: Hunan: Xinshao	PV335154	PV340627	Cai et al. 2025
6	*Plagiopholis blakewayi*	HS 11148	China: Yunnan: Mengzi	MK064686	MK201341	Li et al. 2020
7	*Plagiopholis blakewayi*	10-Jun	China: Yunnan	MK201340	MK064685	Li et al. 2020
8	*Plagiopholis blakewayi*	SYS r002136	China: Yunnan: Wenshan	/	PV340636	Cai et al. 2025
9	*Plagiopholis blakewayi*	SYS r002207	China: Sichuan: Yanbian	PV335163	PV340637	Cai et al. 2025
10	*Plagiopholis nuchalis*	QHU 2024045	China: Yunnan: Xishuangbanna	PV335164	PV340638	Cai et al. 2025
11	*Plagiopholis nuchalis*	MS 853	China: Yunnan: Simao	PV335165	PV340639	Cai et al. 2025
12	*Plagiopholis pluvialis*	HS 09028	China: Sichuan: Mianyang	MK064681	MK201336	Li et al. 2020
13	*Plagiopholis pluvialis*	YBU 13224	China: Guizhou: Tongren	/	KT199002	Zhong et al. 2015
14	*Plagiopholis pluvialis*	EM 1906004	China: Sichuan: Leshan	MW697084	MW697084	Li et al. 2020
15	*Plagiopholis pluvialis*	GP 833	China: Sichuan: Anzhou	/	KT199000	Zhong et al. 2015
16	*Plagiopholis pluvialis*	QHU 2024006	China: Sichuan: Dujiangyan	PV335155	PV340628	Cai et al. 2025
17	*Plagiopholis pluvialis*	QHU 2024007	China: Sichuan: Wenchuan	PV335156	PV340629	Cai et al. 2025
18	*Plagiopholis pluvialis*	CIB XMG 2023001	China: Sichuan: Dujiangyan	PV335157	PV340630	Cai et al. 2025
19	*Plagiopholis pluvialis*	CIB CB2024EMS001	China: Sichuan: Emeishan	PV335158	/	Cai et al. 2025
20	*Plagiopholis pluvialis*	CIB 119370	China: Sichuan: Emeishan	PV335159	PV340632	Cai et al. 2025
21	*Plagiopholis pluvialis*	SYS r002035	China: Guizhou: Bijie	PV335162	PV340635	Cai et al. 2025
22	*Plagiopholis styani*	KIZ 20180002	China: Fujian: Wuyishan: Guadun	PV833807	PV847831	Liu et al. 2025
23	*Plagiopholis styani*	CIB WYS2024001	China: Jiangxi: Yanshan	PV335147	PV340620	Cai et al. 2025
24	*Plagiopholis styani*	ZJFRR 202407001	China: Zhejiang: Huzhou	PV335148	PV340621	Cai et al. 2025
25	*Plagiopholis styani*	ZJFRR 202207001	China: Zhejiang: Hangzhou	PV335149	PV340622	Cai et al. 2025
26	*Pseudoxenodon bambusicola*	SYS r000922	China: Guangdong: Shaoguan: Xiaokeng Town	MK064772	/	Li et al. 2020

Results

The BI and ML analyses produced identical topologies, which were integrated in Fig. 2. The pairwise distances based on CO1 and cyt *b* genes among all species are given in the Suppl. materials S1, S2, respectively.

Phylogenetic analyses recovered a strongly supported monophyletic clade comprising all samples of the genus *Plagiopholis* (BPP 1.00). Within *Plagiopholis*, six well-supported clades were resolved, corresponding to the five currently recognized species plus a newly proposed species from Guangdong. The single Guangdong specimen constitutes a separate, strongly supported lineage (BPP = 0.95; UFB = 82; SH-aLRT = 96.2) that is sister to a clade containing *P. pluvialis* and (*P. acuta* + *P. styani*). The Guangdong specimen exhibits pronounced genetic divergence from all recognized congeners (12.73%–15.88% in CO1, 16.17%–17.54% in cyt *b*), exceeding the interspecific distances observed among the known species (4.87%–19.02% in CO1, 6.50%–20.57% in cyt *b*).

Based on their phylogenetic relationships, genetic differentiation, and morphological distinctiveness (see Taxonomic accounts below), we hypothesize that the single specimen from Guangdong represents a separately evolving lineage and should be described as a new species.

Taxonomic accounts

Plagiopholis maculosa **Qi, Song, Yang, Xu, Fang, Su & Wang, sp. nov.**

https://zoobank.org/7B70CA92-FA40-4E84-B38C-6D6A09548493

Type material. Holotype. SYS r002979, adult female (Figs 3–5A), collected by Rui-Jian Fang and Jun-Rong Su on 23 June 2025 from Tianjingshan National Forest Park (24.687856°N, 113.033517°E; ca 680 m a.s.l.), Nanling National Nature Reserve, Ruyuan County, Shaoguan City, Guangdong Province, China.

Etymology. The specific epithet *maculosa* is the feminine nominative singular of the Latin adjective *maculosus* ("spotted, blotched"), chosen to agree in gender with the feminine generic name *Plagiopholis*. It refers to the distinctive series of irregular blotches along the dorsum of the new species.

Suggested common name. Based on the type locality, we propose the English common name as "Nanling mountain snake", and Chinese formal name as "南岭颈斑蛇" (nánlǐng jǐngbānshé).

Diagnosis. *Plagiopholis maculosa* sp. nov. can be differentiated from its congeners by the combination of the following morphological characters: (1) no loreal; (2) temporals 2+2; (3) maxillary teeth 17 in a single

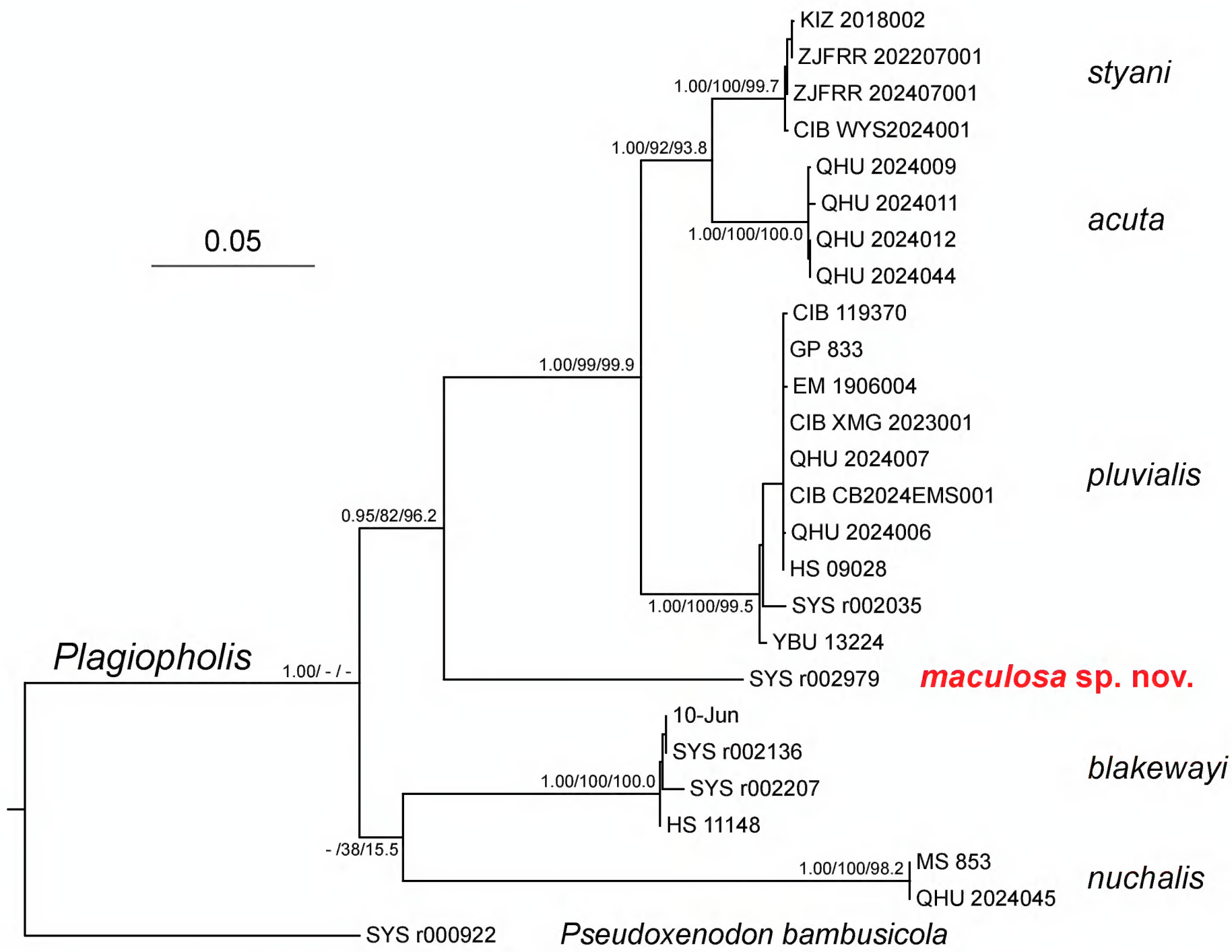

Figure 2. Maximum Likelihood consensus tree inferred from CO1 and cyt *b* genes. Node labels indicate BPP/UFB/SH-aLRT.

female; (4) 104 ventrals, excluding two preventrals in a single female; (5) 24 pairs of subcaudals, excluding tail tip in a single female; (6) presence of a large inverted "V"-shaped nuchal blotch; (7) dorsal surface of the body reddish-brown, with large black-brown spots scattered along the sides; the scales between these lateral spots have white margins, while the anterior and posterior adjacent scales are darker with black-brown edges, together forming irregular blotches along the dorsum.

Description of holotype. Adult female (Figs 3–5A, 6A). Body size small and stubby, TL 295.9 mm (SVL 261.4 mm, TaL 34.5 mm), tail short (TaL/TL: 0.12). Head small, indistinct from neck, longer than width and narrow anteriorly, HL 13.3 mm, HW 8.4 mm (HW/HL: 0.63); eye relative moderate, ED 2.4 mm (ED/HL: 0.18), pupil round. Rostral triangular, much wider than high, visible from dorsum; nostril laterally pointed, located in the middle of nasal; nasal divided into two scales by nostril; no loreal; postnasal in contact with one enlarged preocular; two postoculars, upper one larger than the lower; two anterior temporals and two posterior temporals on each side; six supralabials on each side, first and second in contact with nasal, fourth and fifth entering the orbit, the sixth largest; two pairs of chin shields, elongate, the anterior pair in contact with the mental and slightly longer than posterior one; six infralabials on each side, first to third in contact with anterior pair of chin shields, third and forth in contact with posterior chin shields; internasals and prefrontals paired; frontal single and enlarged, narrowed posteriorly; parietals paired, longer than width, in contact with each other medially, with upper anterior and posterior temporals laterally. Dorsal scales in 15–15–15 rows, smooth throughout, without apical pits, the outermost dorsal scale rows are enlarged and significantly differ in size from adjacent scales; 104 ventrals, excluding two preventrals; 24 pairs of subcaudals, excluding tail tip; precloacal plate entire.

Coloration in life. Dorsal surface of head reddish-brown, with scattered small black spots and brown blotches; the supralabials and infralabials are creamy-white with black and brown edges on both sides. Ventral surface of head cream-white, with scattered large irregular black-brown blotches on the throat. A large, black-brown, inverted "V"-shaped nuchal blotch is present on the neck, across eight scales at its widest point, across two or three scales on each side, with its posterior margin faintly tinged with yellow. Dorsal surface of the body reddish-brown, with large black-brown spots scattered along the sides; the scales between these lateral spots have white margins, while the anterior and posterior adjacent scales are darker with black-brown edges, together form-

Figure 3. The holotype of *Plagiopholis maculosa* sp. nov. in life. **A.** Dorsolateral view of body; **B.** Ventral view of body; **C.** Dorsal head; **D.** Lateral head; **E.** Ventral head. Photos by Shuo Qi and Hao-Cong Yang.

Figure 4. The holotype of *Plagiopholis maculosa* sp. nov. in preservation. **A.** Dorsol view of body; **B.** Ventral view of body. Photos by Shuo Qi.

ing irregular blotches along the dorsum. The ventral surface of the neck is cream-white in ground color, bearing brown blotches edged with black. The ventral coloration of the body is slightly darker, composed of numerous orange-red pigment spots, with some ventral scales bearing larger dark brown blotches on both sides. The ventral surface of the tail is slightly yellowish.

Coloration in preservation. The coloration of the dorsum faded to grayish brown. The irregular blotches on the dorsum became more distinct. The ventral surface faded to yellowish white.

Comparisons. *Plagiopholis maculosa* sp. nov. is distinguishable from its congeners by a combination of the following morphological characters (Table 2; Figs 5; 6).

Figure 5. Comparisons of general morphological aspect among all *Plagiopholis* species in China. **A.** *Plagiopholis maculosa* sp. nov., from Ruyuan County, Guangdong Province, photo by Hao-Cong Yang; **B.** *Plagiopholis acuta*, from Xinshao County, Hunan Province, photo by Yu-Hao Xu; **C.** *Plagiopholis blakewayi*, from Yanbian County, Sichuan Province, photo by Jian Wang; **D.** *Plagiopholis nuchalis*, from Dai Autonomous Prefecture of Xishuangbanna, Yunnan Province, photo by Tie-Rui Zhang; **E.** *Plagiopholis pluvialis*, from Wenchuan County, Sichuan Province, photo by Yu-Hao Xu; **F.** *Plagiopholis styani*, from Lin'an District, Zhejiang Province, photo by Yu-Hao Xu.

Table 2. Diagnostic characters among all seven species of the genus *Plagiopholis*.

Species	SPL	IFL	LoR	PrO	PtO	TMP	V	SC	MT	NB	Reference
Plagiopholis maculosa sp. nov.	6	6	0	1	2	2+2	104 in a single female	24 in a single female	17 in a single female	inverted "V"-shaped	This study
Plagiopholis acuta	6, rarely 7	6	0	1	2	2+2,	114–115 in males; 115–121 in females	29–30 in males; 24–25 in females	17–18 in males; 15–17 in females	pentagonal or sub-annular shaped	Cai et al. (2025)
Plagiopholis blakewayi	5 or 6	6, rarely 4 or 5	0, rarely 1	1	2, rarely 1	0+1 or 1+1	107–125 in males; 115–132 in females	20–31 in males; 17–28 in females	n/a	arrow-shaped, irregular, or absent	Zhao (2006); Huang (2021)
Plagiopholis delacouri	6	n/a	n/a	1	2	1+2	113–129	22–28	n/a	inverted "V"-shaped	Angel (1929)
Plagiopholis nuchalis	6	6	1	1	2	1+2	122–142	23–30	20–22	inverted "V"-shaped	Zhao (2006)
Plagiopholis pluvialis	6	6	0, rarely 1	1	2	2+2, rarely 2+1	102–110 in males;114–122 in females	26–31 in males; 16–26 in females	18 in males	inverted "V"-shaped	Cai et al. (2025)
Plagiopholis styani	6, rarely 7	6, rarely 5	0, rarely 1	1	2	2+2, rarely 2+1	114–121 in males; 116–122 in females	26–30 in males; 23–28 in females	20–21 in males; around 18 in female	pentagonal, sub-annular or sagittate shaped	Liu et al. (2025); Cai et al. (2025)

By absence of the loreal, *Plagiopholis maculosa* sp. nov. can be distinguished from *P. nuchalis* (single loreal).

By having temporal scales 2+2, *Plagiopholis maculosa* sp. nov. can be distinguished from *P. blakewayi* (0/1+1), *P. nuchalis* (1+2), and *P. delacouri* (1+2).

By having fewer ventral scales (104 in the single female), *Plagiopholis maculosa* sp. nov. can be distinguished from *P. acuta* (114–115 in males; 115–121 in females), *P. blakewayi* (107–125 in males; 115–132 in females), *P. delacouri* (113–129), *P. nuchalis* (122–142), *P. pluvialis* (102–110 in males; 114–122 in females), *P. styani* (114–121 in males; 116–122 in females).

By having a large inverted "V"-shaped nuchal blotch, *Plagiopholis maculosa* sp. nov. can be distinguished from *P. acuta* (pentagonal or sub-annular shaped) and *P. styani* (pentagonal, sub-annular or sagittate shaped).

By having a series of irregular blotches on the dorsum, *Plagiopholis maculosa* sp. nov. can be distinguished from all congeners (reticulated pattern on the dorsum).

Distribution and ecology. *Plagiopholis maculosa* sp. nov. is currently known only from Tianjingshan National Forest Park, Nanling National Nature Reserve, Ruyuan County, Shaoguan City, Guangdong Province, China. The holotype was discovered at approximately 9:00 a.m. in a roadside ditch within evergreen broad-leaved forest at an elevation of ca. 680 m. The forest is characterized by dense canopy cover, abundant leaf litter, and a moist microenvironment typical of the Nanling Mountains region.

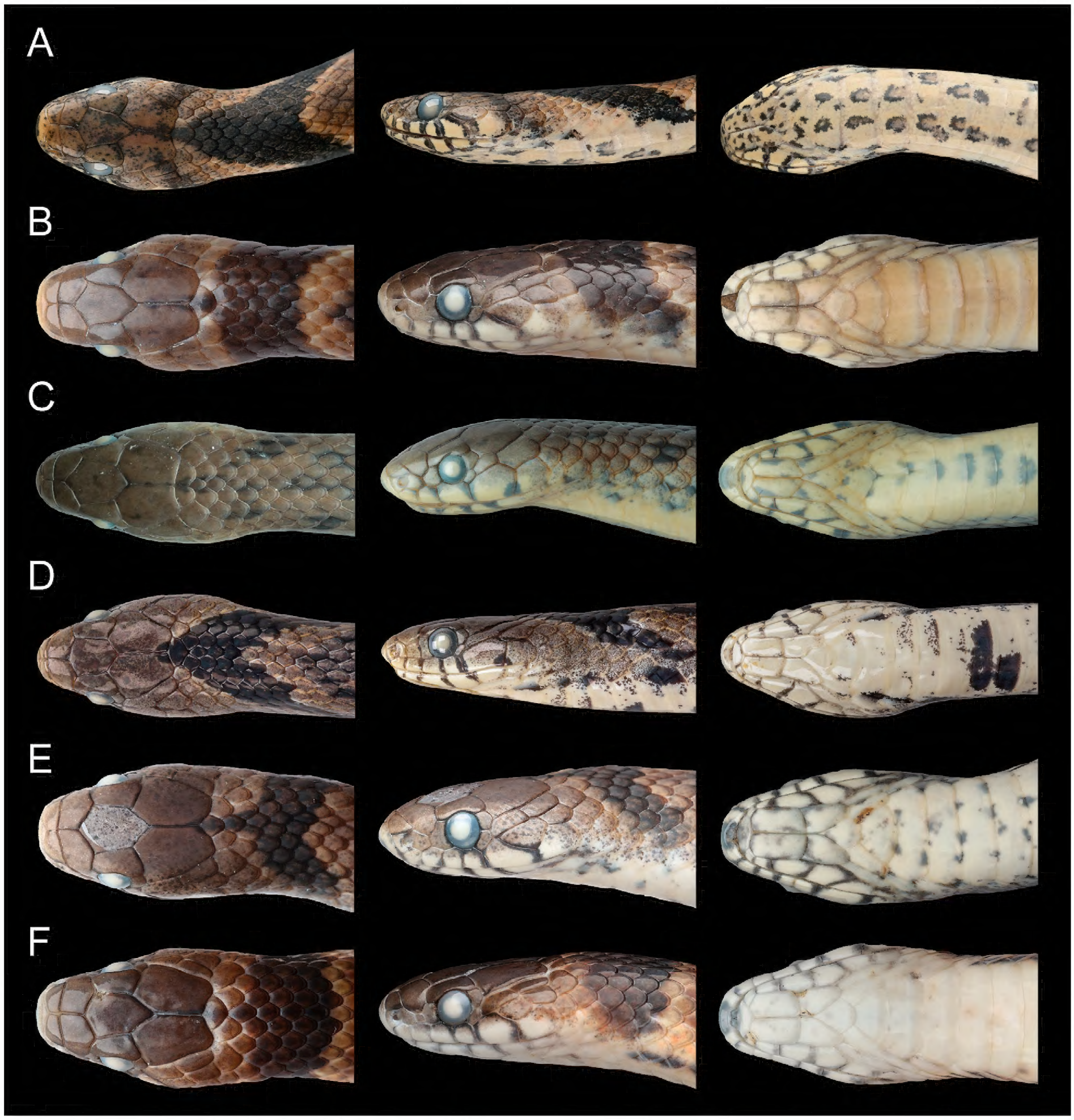

Figure 6. Dorsal (left), lateral (middle), and ventral (right) head comparisons among *Plagiopholis* species in China. **A.** *Plagiopholis maculosa* sp. nov., SYS r002929, from Mt. Tianjing, Guangdong Province, Photos by Shuo Qi; **B.** *P. acuta*, QHU 2024009, from Xinshao County, Hunan Province, Photos by Yu-Hao Xu; **C.** *P. blakewayi*, QHU R2024056, from Liupanshui City, Guizhou Province, Photos by Yu-Hao Xu; **D.** *P. nuchalis*, ANU ZR24067, from Xishuangbanna, Yunnan Province, Photos by Tie-Rui Zhang; **E.** *P. pluvialis*, QHU 2024007, from Dujiangyan, Sichuan Province, Photos by Yu-Hao Xu; **F.** *P. styani*, ZJFRR 2022001, from Lin'an District, Zhejiang Province, Photos by Yu-Hao Xu. Images are not to scale.

Discussion

The Nanling Mountains, situated at the junction of several major biogeographic regions of southern China, function as both a refugium and a dispersal corridor. Recognized as a biodiversity hotspot harboring unique amphibian and reptile lineages, the discovery of *Plagiopholis maculosa* provides additional evidence of the region's remarkable faunal diversity and biogeographic significance. Although *P. maculosa* is described based on a single specimen, both morphological distinctiveness and significant genetic divergence from all congeners provide sufficient evidence to justify its recognition as a valid species. The rarity of *Plagiopholis* in field collections may be attributed to its secretive habits, narrow habitat preference, and low population density, which together explain the scarcity of available specimens.

Liang (2003) reported a new record of *Plagiopholis styani* from Guangdong Province, describing its nuchal

marking as a black transverse band. This feature differs from that of *P. maculosa* described herein, but corresponds to the diagnostic characters of *P. acuta* and *P. styani*. Therefore, pending the acquisition of additional specimens, the distribution record of *P. styani* in Guangdong is retained.

Despite recent advances in the systematics of *Plagiopholis* (Zhong et al. 2015; Cai et al. 2025; Liu et al. 2025; this study), the genus still suffers from significant sampling gaps. Nearly all molecular data available so far have been derived from Chinese populations, while no genetic data are available from Myanmar, Laos, Vietnam, or Thailand. Consequently, the taxonomic status of *P. delacouri* from Vietnam and Laos remains uncertain, and the possibility of cryptic lineages within populations from Myanmar and Thailand cannot be ruled out. Comprehensive sampling across the full distribution of the genus is therefore essential. Such efforts will provide a more complete understanding of its species diversity and evolutionary history.

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Supplementary material 1

Uncorrected p distances (%) of the CO1 gene amongst species of genus *Plagiopholis*

Authors: Shuo Qi, Han-Ming Song, Hao-Cong Yang, Yu-Hao Xu, Rui-Jian Fang, Jun-Rong Su, Zhi-Fa Liu, Yue-Ning Gong, Fang-Hua Li, Chun-He Lyu, Bing-Yang Wang, Ying-Yong Wang

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Link: https://doi.org/10.3897/zse.101.172706.suppl1

Supplementary material 2

Uncorrected p distances (%) of the cyt b gene amongst species of genus *Plagiopholis*

Authors: Shuo Qi, Han-Ming Song, Hao-Cong Yang, Yu-Hao Xu, Rui-Jian Fang, Jun-Rong Su, Zhi-Fa Liu, Yue-Ning Gong, Fang-Hua Li, Chun-He Lyu, Bing-Yang Wang, Ying-Yong Wang

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